

LOCUS MAU18263 1665 bp DNA linear BCT 26-OCT-1995  
 DEFINITION Mycobacterium avium alkyl hydroperoxidase C (ahpC) gene, complete cds, and OxyR homolog gene, complete cds.  
 ACCESSION U18263  
 VERSION U18263.1 GI:1040852  
 SOURCE Mycobacterium avium  
 ORGANISM Mycobacterium avium  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).  
 REFERENCE 1 (bases 1 to 1665)  
 AUTHORS Sherman,D.R., Sabo,P.J., Hickey,M.J., Arain,T.M., Mahairas,G.G., Yuan,Y., Barry,C.E. III and Stover,C.K.  
 TITLE Disparate responses to oxidative stress in saprophytic and pathogenic mycobacteria  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (14), 6625-6629 (1995)  
 REFERENCE 2 (bases 1 to 771)  
 AUTHORS Yamaguchi,R., Matsuo,K., Yamazaki,A., Takahashi,M., Fukasawa,Y., Wada,M. and Abe,C.  
 TITLE Cloning and expression of the gene for the Avi-3 antigen of Mycobacterium avium and mapping of its epitopes  
 JOURNAL Infect. Immun. 60 (3), 1210-1216 (1992)  
 REFERENCE 3 (bases 1 to 1665)  
 AUTHORS Hickey,M.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-DEC-1994) Mark J. Hickey, TB & Molecular Microbiology, PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA

Query Match 14.1%; Score 235.8; DB 1; Length 1665;  
 Best Local Similarity 55.3%; Pred. No. 5.7e-48;  
 Matches 506; Conservative 0; Mismatches 397; Indels 12; Gaps 2;

Qy 469 ATTCACCGTTATAGTTATAGGCATGAGCAATAAAGAGTACCGGCCCACACTCGCCCAGCT 528  
 ||| || ||| ||||| ||| |||| ||| ||||| ||||| ||  
 Db 682 ATTTCCCACTACACTTATAGGTATGCCCAGATAAGACTTATCAGCCCACGATCGCCGGCCT 741  
 Qy 529 TCGCACCTTTGTCCACCATCGCAGAATGCAAGCACTTTGGTACTGCTGCCACCAAGCTGTC 588  
 ||| |||| ||| ||||| || |||| || |||| |||| ||  
 Db 742 GCGCGCCTTCGTGCGGGTCGCCGAGAAGCGCCAATTCAGCGGTGCCGCAACGGCTTTGGG 801  
 Qy 589 CATTTCGCAGCCATCCCTCTCCAGGCACTTGTCGCATTAGAAACAGGCCTGGGAGTTCA 648  
 | ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
 Db 802 AGTCAGCCAGTCGACGCTGTGCGAGGTGTTGGCGGCGCTGGAGGCGGGGCTGGGCACGCA 861  
 Qy 649 GCTGATTGAACGCTCCACCCGCAAGGTCATTGTACCCCCAGCGGGCGAGAAGTTGCTGCC 708  
 ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
 Db 862 GTTGGTGGAGCGCTCCACCCGGCGTGTCTTCTTGACACCCAGGGCGCCGAGCTGCTGCC 921  
 Qy 709 ATTCGCCAAATCCACCCTTGACGCGGCGGAGTCTTTCCTCTCCACGCCAAGGGCGCCAA 768  
 |||| | || ||||| || |||| | || |||| | ||  
 Db 922 GCACGCCAGGCCGTGGTCGAGGCGGCCGACGCCTTACCGCGGCGGCGGGGTTCGAC 981  
 Qy 769 CGGTTCGCTCACTGGACCGTTGACCGTAGGCATCATCCCCACGGCGGCTCCTTACATTTT 828  
 | ||| || ||||| || ||||| ||||| ||||| ||||| ||||| ||  
 Db 982 GGACCCGTTGCGGGCCGGCATGCGGCTGGGGCTGATCCCCACGGTGGTGCCCTACGTGCT 1041

Qy	829	GCCGTCAATGCTGTCCATCGTGGATGAAGAATATCCAGATCTGGAACCTCACATCGTCTGA	888
Db	1042	GCCGACCGTGCTGGCCGGAATCGCCGAACGGCGGCCCGGCCTGACCCTGCGGGTCACCGA	1101
Qy	889	GGACCAAACCAAGCATCTTCTCGCGTTGCTGCGCGACGGCGCCATCGACGTCGCCATGAT	948
Db	1102	GGACCAGACCGAACGGCTGCTGGCGGTGCTGCGCGAGGGCGCCCTCGACGCGGCGCTGAT	1161
Qy	949	GGCCCTGCCTTCTGAGGCAACAGGCATGAAGGAAATCCCCCTCTACGACGAAGACTTTAT	1008
Db	1162	CGCGCTGCCCCGCCGAGACGGCGGGCGTCAACGCGATCCCCTCTACGACGAGGATTTCTG	1221
Qy	1009	CGTCGTTACAGCTAGCGATCACCCCTTCGCCGGCCGCCAAGACTTAGAACTATCCGCCTT	1068
Db	1222	GCTCGCGCTTCCGCCGGGCCACCCGCTGGCGGGCAAGCGCCGGGTGCCGGCGACGGCGCT	1281
Qy	1069	AGAAGACCTCGATCTGCTGCTTCTCGACGACGGACACTGCCTCCACGACCAAATTGTGGA	1128
Db	1282	GGCCGACCTGCCGCTGCTGCTGCTGGACGAGGGGCACTGCCTGCGCGACCAGGCGCTGGA	1341
Qy	1129	CCTGTGCCGCCGCGGAGACATCAACCCATTAGCTCCACTACTGCTGTCACCCGCGCATC	1188
Db	1342	CGTCTGCCACAAGGCGGGTGTGCGGGCGGAGCTGGCCAAT-----ACCCGGGCCGC	1392
Qy	1189	CAGCCTTACCACCGTCATGCAGCTCGTCGTCGCCGGCCTTGGATCCACCTTGGTCCCAAT	1248
Db	1393	CTCGCTGGCCACCGCGGTGCAGTGCCTGACCGGCGGCCTGGGGGTGACGCTCATCCCGCA	1452
Qy	1249	CAGCGCAATCCCATGGGAATGCACCCGACCAGGACTGGCAACAGCCAACTTCAACTCTGA	1308
Db	1453	GAGCGCGGTCCCGGTGGAGGCGTCGCGCAGCCGGCTGGGCCTGGCCAGTTCCGCCGCGCC	1512
Qy	1309	TGTCACCGCAAACCGCCGCATTGGATTGGTGTACCGTTCCTCTTCTCTCGCGCCGAAGA	1368
Db	1513	GCGCCCGG---GCCGGCGCATCGGCTGGTGTTCGCTCGTCGAGCGGGCGCGACGACTC	1569
Qy	1369	GTTCGAACAGTTTGC	1383
Db	1570	CTACCGCGAGCTGGC	1584